



1102-98.TXT

SEQUENCE LISTING

<110> Kainoh, Mie
Tanaka, Toshiaki

<120> Chimeric Proteins, their Heterodimer Complexes, and Platelet Substitutes

<130> 1102-98

<140> 09/155,514
<141> 1998-11-17

<150> WO PCT/JP98/00370
<151> 1998-01-29

<150> JP 9-15118
<151> 1997-01-29

<150> JP-9-234544
<151> 1997-08-29

<160> 34

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 4228
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence encoding fusion protein

<221> CDS
<222> (1)...(2958)

<221> CDS
<222> (3316)...(3360)

<221> CDS
<222> (3480)...(3808)

<221> CDS
<222> (3905)...(4228)

<400> 1
atg ttc ccc acc gag agc gca tgg ctt ggg aag cga ggc gcg aac ccg 48
Met Phe Pro Thr Glu Ser Ala Trp Leu Gly Lys Arg Gly Ala Asn Pro
1 5 10 15

ggc ccc gaa gct gca ctc cgg gag acg gtg atg ctg ttg ctg tgc ctg 96
Gly Pro Glu Ala Ala Leu Arg Glu Thr Val Met Leu Leu Leu Cys Leu
20 25 30

ggg gtc ccg acc ggc agg cct tac aac gtg gac act gag agc gcg ctg 144
Gly Val Pro Thr Gly Arg Pro Tyr Asn Val Asp Thr Glu Ser Ala Leu
35 40 45

ctt tac cag ggc ccc cac aac acg ctg ttc ggc tac tcg gtc gtg ctg 192

1102-98.TXT

Leu	Tyr	Gln	Gly	Pro	His	Asn	Thr	Leu	Phe	Gly	Tyr	Ser	Val	Val	Leu	
50					55					60						
cac	agc	cac	ggg	gcg	aac	cga	tgg	ctc	cta	gtg	ggt	gcg	ccc	act	gcc	240
His	Ser	His	Gly	Ala	Asn	Arg	Trp	Leu	Leu	Val	Gly	Ala	Pro	Thr	Ala	
65					70					75					80	
aac	tgg	ctc	gcc	aac	gct	tca	gtg	atc	aat	ccc	ggg	gcg	att	tac	aga	288
Asn	Trp	Leu	Ala	Asn	Ala	Ser	Val	Ile	Asn	Pro	Gly	Ala	Ile	Tyr	Arg	
									90					95		
tgc	agg	atc	gga	aag	aat	ccc	ggc	cag	acg	tgc	gaa	cag	ctc	cag	ctg	336
Cys	Arg	Ile	Gly	Lys	Asn	Pro	Gly	Gln	Thr	Cys	Glu	Gln	Leu	Gln	Leu	
								105					110			
ggt	agc	cct	aat	gga	gaa	cct	tgt	gga	aag	act	tgt	ttg	gaa	gag	aga	384
Gly	Ser	Pro	Asn	Gly	Glu	Pro	Cys	Gly	Lys	Thr	Cys	Leu	Glu	Glu	Arg	
								120				125				
gac	aat	cag	tgg	ttg	ggg	gtc	aca	ctt	tcc	aga	cag	cca	gga	gaa	aat	432
Asp	Asn	Gln	Trp	Leu	Gly	Val	Thr	Leu	Ser	Arg	Gln	Pro	Gly	Glu	Asn	
								135			140					
gga	tcc	atc	gtg	act	tgt	ggg	cat	aga	tgg	aaa	aat	ata	ttt	tac	ata	480
Gly	Ser	Ile	Val	Thr	Cys	Gly	His	Arg	Trp	Lys	Asn	Ile	Phe	Tyr	Ile	
								150			155				160	
aag	aat	gaa	aat	aag	ctc	ccc	act	ggt	ggt	tgc	tat	gga	gtg	ccc	cct	528
Lys	Asn	Glu	Asn	Lys	Leu	Pro	Thr	Gly	Gly	Cys	Tyr	Gly	Val	Pro	Pro	
								165			170			175		
gat	tta	cga	aca	gaa	ctg	agt	aaa	aga	ata	gct	ccg	tgt	tat	caa	gat	576
Asp	Leu	Arg	Thr	Glu	Leu	Ser	Lys	Arg	Ile	Ala	Pro	Cys	Tyr	Gln	Asp	
								180			185			190		
tat	gtg	aaa	aaa	ttt	gga	gaa	aat	ttt	gca	tca	tgt	caa	gct	gga	ata	624
Tyr	Val	Lys	Lys	Phe	Gly	Glu	Asn	Phe	Ala	Ser	Cys	Gln	Ala	Gly	Ile	
								195			200			205		
tcc	agt	ttt	tac	aca	aag	gat	tta	att	gtg	atg	ggg	gcc	cca	gga	tca	672
Ser	Ser	Phe	Tyr	Thr	Lys	Asp	Leu	Ile	Val	Met	Gly	Ala	Pro	Gly	Ser	
								210			215			220		
tct	tac	tgg	act	ggc	tct	ctt	ttt	gtc	tac	aat	ata	act	aca	aat	aaa	720
Ser	Tyr	Trp	Thr	Gly	Ser	Leu	Phe	Val	Tyr	Asn	Ile	Thr	Thr	Asn	Lys	
								225			230			235		
tac	aag	gct	ttt	tta	gac	aaa	caa	aat	caa	gta	aaa	ttt	gga	agt	tat	768
Tyr	Lys	Ala	Phe	Leu	Asp	Lys	Gln	Asn	Gln	Val	Lys	Phe	Gly	Ser	Tyr	
								245			250			255		
tta	gga	tat	tca	gtc	gga	gct	ggt	cat	ttt	cg	agc	cag	cat	act	acc	816
Leu	Gly	Tyr	Ser	Val	Gly	Ala	Gly	His	Phe	Arg	Ser	Gln	His	Thr	Thr	
								260			265			270		
gaa	gta	gtc	gga	gga	gct	cct	caa	cat	gag	cag	att	ggt	aag	gca	tat	864
Glu	Val	Val	Gly	Gly	Ala	Pro	Gln	His	Glu	Gln	Ile	Gly	Lys	Ala	Tyr	
								275			280			285		
ata	ttc	agc	att	gat	gaa	aaa	gaa	cta	aat	atc	tta	cat	gaa	atg	aaa	912
Ile	Phe	Ser	Ile	Asp	Glu	Lys	Glu	Leu	Asn	Ile	Leu	His	Glu	Met	Lys	
								290			295			300		

1102-98.TXT

ggt aaa aag ctt gga tcg tac ttt gga	305	310	315	320	960
Gly Lys Lys Leu Gly Ser Tyr Phe Gly Ala Ser Val Cys Ala Val Asp					
ctc aat gca gat ggc ttc tca gat ctg					1008
Leu Asn Ala Asp Gly Phe Ser Asp Leu	325	330	335		
ctc gta atg aat gca atg gaa aca aac					1056
Ser Thr Ile Arg Glu Glu Gly Arg Val	340	345	350		
tcg gga gca gta atg aat gca atg gaa					1104
Ser Gly Ala Val Met Asn Ala Met Glu	355	360	365		
aaa tat gct gca aga ttt ggg gaa tct	370	375	380		1152
Lys Tyr Ala Ala Arg Phe Gly Glu Ser					
gac aat gat ggc ttt gaa gat gtt gct					1200
Asp Asn Asp Gly Phe Glu Asp Val Ala	385	390	395		
gac ttg caa ggt gct att tat att tac					1248
Asp Leu Gln Gly Ala Ile Tyr Ile Tyr	405	410	415		
tcg tca acc ttc tca cag aga att gaa					1296
Ser Ser Thr Phe Ser Gln Arg Ile Glu	420	425	430		
tta agt atg ttt gga cag tct ata tca					1344
Leu Ser Met Phe Gly Gln Ser Ile Ser	435	440	445		
aat ggc tat gta gat gta gca gtt ggt					1392
Asn Gly Tyr Val Asp Val Ala Val Gly	450	455	460		
gtc ttg cta agg aca aga cct gta gta					1440
Val Leu Leu Arg Thr Arg Pro Val Val	465	470	475		
cac cct gag tca gta aat aga acg aaa					1488
His Pro Glu Ser Val Asn Arg Thr Lys	485	490	495		
tgg cct tct gtg tgc ata gat cta aca					1536
Trp Pro Ser Val Cys Ile Asp Leu Thr	500	505	510		
aag gaa gtt cca ggt tac att gtt ttg					1584
Lys Glu Val Pro Gly Tyr Ile Val Leu	515	520	525		
gtg aac aga aag gca gag tct cca cca					1632
Val Asn Arg Lys Ala Glu Ser Pro Pro	530	535	540		
gga act tct gac gtg att aca gga agc					1680
Gly Thr Ser Asp Val Ile Thr Gly Ser	545	550	555		

1102-98.TXT

gct aac tgt aga aca cat caa gca ttt atg cgg aaa gat gtg cg ^g gac	1728
Ala Asn Cys Arg Thr His Gln Ala Phe Met Arg Lys Asp Val Arg Asp	
565 570 575	
atc ctc acc cca att cag att gaa gct gct tac cac ctt ggt cct cat	1776
Ile Leu Thr Pro Ile Gln Ile Glu Ala Ala Tyr His Leu Gly Pro His	
580 585 590	
gtc atc agt aaa cga agt aca gag gaa ttc cca cca ctt cag cca att	1824
Val Ile Ser Lys Arg Ser Thr Glu Glu Phe Pro Pro Leu Gln Pro Ile	
595 600 605	
ctt cag cag aag aaa gaa aaa gac ata atg aaa aaa aca ata aac ttt	1872
Leu Gln Gln Lys Lys Glu Lys Asp Ile Met Lys Lys Thr Ile Asn Phe	
610 615 620	
gca agg ttt tgt gcc cat gaa aat tgt tct gct gat tta cag gtt tct	1920
Ala Arg Phe Cys Ala His Glu Asn Cys Ser Ala Asp Leu Gln Val Ser	
625 630 635 640	
gca aag att ggg ttt ttg aag ccc cat gaa aat aaa aca tat ctt gct	1968
Ala Lys Ile Gly Phe Leu Lys Pro His Glu Asn Lys Thr Tyr Leu Ala	
645 650 655	
gtt ggg agt atg aag aca ttg atg ttg aat gtg tcc ttg ttt aat gct	2016
Val Gly Ser Met Lys Thr Leu Met Leu Asn Val Ser Leu Phe Asn Ala	
660 665 670	
gga gat gat gca tat gaa acg act cta cat gtc aaa cta ccc gtg ggt	2064
Gly Asp Asp Ala Tyr Glu Thr Thr Leu His Val Lys Leu Pro Val Gly	
675 680 685	
ctt tat ttc att aag att tta gag ctg gaa gag aag caa ata aac tgt	2112
Leu Tyr Phe Ile Lys Ile Leu Glu Leu Glu Glu Lys Gln Ile Asn Cys	
690 695 700	
gaa gtc aca gat aac tct ggc gtg gta caa ctt gac tgc agt att ggc	2160
Glu Val Thr Asp Asn Ser Gly Val Val Gln Leu Asp Cys Ser Ile Gly	
705 710 715 720	
tat ata tat gta gat cat ctc tca agg ata gat att agc ttt ctc ctg	2208
Tyr Ile Tyr Val Asp His Leu Ser Arg Ile Asp Ile Ser Phe Leu Leu	
725 730 735	
gat gtg agc tca ctc agc aga gcg gaa gag gac ctc agt atc aca gtg	2256
Asp Val Ser Ser Leu Ser Arg Ala Glu Glu Asp Leu Ser Ile Thr Val	
740 745 750	
cat gct acc tgt gaa aat gaa gag gaa atg gac aat cta aag cac agc	2304
His Ala Thr Cys Glu Asn Glu Glu Glu Met Asp Asn Leu Lys His Ser	
755 760 765	
aga gtg act gta gca ata cct tta aaa tat gag gtt aag ctg act gtt	2352
Arg Val Thr Val Ala Ile Pro Leu Lys Tyr Glu Val Lys Leu Thr Val	
770 775 780	
cat ggg ttt gta aac cca act tca ttt gtg tat gga tca aat gat gaa	2400
His Gly Phe Val Asn Pro Thr Ser Phe Val Tyr Gly Ser Asn Asp Glu	
785 790 795 800	
aat gag cct gaa acg tgc atg gtg gag aaa atg aac tta act ttc cat	2448
Asn Glu Pro Glu Thr Cys Met Val Glu Lys Met Asn Leu Thr Phe His	

1102-98.TXT

805

810

815

gtt atc aac act ggc aat agt atg gct ccc aat gtt agt gtg gaa ata	2496
Val Ile Asn Thr Gly Asn Ser Met Ala Pro Asn Val Ser Val Glu Ile	
820 825 830	
atg gta cca aat tct ttt agc ccc caa act gat aag ctg ttc aac att	2544
Met Val Pro Asn Ser Phe Ser Pro Gln Thr Asp Lys Leu Phe Asn Ile	
835 840 845	
ttg gat gtc cag act act act gga gaa tgc cac ttt gaa aat tat caa	2592
Leu Asp Val Gln Thr Thr Gly Glu Cys His Phe Glu Asn Tyr Gln	
850 855 860	
aga gtg tgt gca tta gag cag caa aag agt gca atg cag acc ttg aaa	2640
Arg Val Cys Ala Leu Glu Gln Gln Lys Ser Ala Met Gln Thr Leu Lys	
865 870 875 880	
ggc ata gtc cgg ttc ttg tcc aag act gat aag agg cta ttg tac tgc	2688
Gly Ile Val Arg Phe Leu Ser Lys Thr Asp Lys Arg Leu Leu Tyr Cys	
885 890 895	
ata aaa gct gat cca cat tgt tta aat ttc ttg tgt aat ttt ggg aaa	2736
Ile Lys Ala Asp Pro His Cys Leu Asn Phe Leu Cys Asn Phe Gly Lys	
900 905 910	
atg gaa agt gga aaa gaa gcc agt gtt cat atc caa ctg gaa ggc cgg	2784
Met Glu Ser Gly Lys Glu Ala Ser Val His Ile Gln Leu Glu Gly Arg	
915 920 925	
cca tcc att tta gaa atg gat gag act tca gca ctc aag ttt gaa ata	2832
Pro Ser Ile Leu Glu Met Asp Glu Thr Ser Ala Leu Lys Phe Glu Ile	
930 935 940	
aga gca aca ggt ttt cca gag cca aat cca aga gta att gaa cta aac	2880
Arg Ala Thr Gly Phe Pro Glu Pro Asn Pro Arg Val Ile Glu Leu Asn	
945 950 955 960	
aag gat gag aat gtt gcg cat gtt cta ctg gaa gga cta cat cat caa	2928
Lys Asp Glu Asn Val Ala His Val Leu Leu Glu Gly Leu His His Gln	
965 970 975	
aga ccc aaa cgt tat ttc acg gat ccc gag ctgctggaaag caggctcagc	2978
Arg Pro Lys Arg Tyr Phe Thr Asp Pro Glu	
980 985	
gctccgcct ggacgcattcc cggctatgca gccccagtc agggcagcaa ggcaggcccc	3038
gtctgcctct tcacccggag cctctgccc ccccactcat gctcagggag agggtcttct	3098
ggcttttcc caggctctgg gcaggcacag gctaggtgcc cctaaccagg gcccgcaca	3158
caaaggggca ggtgctgggc tcagacctgc caagagccat atccgggagg accctgcccc	3218
tgacctaagc ccaccccaa ggccaaactc tccactccct cagctcggac accttctctc	3278
ctcccaagatt ccagtaactc ccaatcttct ctctgc aag ccc aaa tct tgt gac	3333
Glu Pro Lys Ser Cys Asp	
990	
aaa act cac aca tgc cca ccg tgc cca ggtaagccag cccaggcctc	3380
Lys Thr His Thr Cys Pro Pro Cys Pro	
995 1000	
gccctccagc tcaaggcggg acaggtgccc tagagtagcc tgcattcagg gacaggcccc	3440
agccgggtgc tgacacgtcc acctccatct cttcctcag cac ctg aac tcc tgg	3494
His Leu Asn Ser Trp	
1005	

1102-98.TXT

ggg gac cgt cag tct tcc tct tcc ccc caa aac cca agg aca ccc tca Gly Asp Arg Gln Ser Ser Ser Ser Pro Gln Asn Pro Arg Thr Pro Ser 1010 1015 1020	3542
tga tct ccc gga ccc ctg agg tca cat gcg tgg tgg tgg acg tga gcc * Ser Pro Gly Pro Leu Arg Ser His Ala Trp Trp Trp Thr * Ala 1025 1030 1035	3590
acg aag acc ctg agg tca agt tca act ggt acg tgg acg gcg tgg agg Thr Lys Thr Leu Arg Ser Ser Thr Gly Thr Trp Thr Ala Trp Arg 1040 1045 1050	3638
tgc ata atg cca aga caa agc cgc ggg agg agc agt aca aca gca cgt Cys Ile Met Pro Arg Gln Ser Arg Gly Arg Ser Ser Thr Thr Ala Arg 1055 1060 1065	3686
acc ggg tgg tca gcg tcc tca ccg tcc tgc acc agg act gcc tga atg Thr Gly Trp Ser Ala Ser Ser Pro Ser Cys Thr Arg Thr Gly * Met 1070 1075 1080	3734
gca agg agt aca agt gca agg tct cca aca aag ccc tcc cag ccc cca Ala Arg Ser Thr Ser Ala Arg Ser Pro Thr Lys Pro Ser Gln Pro Pro 1085 1090 1095	3782
tcg aga aaa cca tct cca aag cca aa ggtgggaccc gtggggtgcg Ser Arg Lys Pro Ser Pro Lys Pro Lys 1100 1105	3828
agggccacat ggacagaggc cggctcgcc caccctctgc cctgagagtg accgctgtac caacctctgt cctaca g ggc agc ccc gag aac cac agg tgt aca ccc tgc Gly Ser Pro Glu Asn His Arg Cys Thr Pro Cys 1110 1115	3888 3938
ccc cat ccc ggg atg agc tga cca aga acc agg tca gcc tga cct gcc Pro His Pro Gly Met Ser * Pro Arg Thr Arg Ser Ala * Pro Ala 1120 1125 1130	3986
tgg tca aag gct tct atc cca gcg aca tcg ccg tgg agt ggg aga gca Trp Ser Lys Ala Ser Ile Pro Ala Thr Ser Pro Trp Ser Gly Arg Ala 1135 1140 1145	4034
atg ggc agc cgg aga aca act aca aga cca cgc ctc ccg tgc tgg att Met Gly Ser Arg Arg Thr Thr Arg Pro Arg Leu Pro Cys Trp Ile 1150 1155 1160 1165	4082
ccg acg gct cct tct tcc tct aca gca agc tca ccg tgg aca aga gca Pro Thr Ala Pro Ser Ser Ser Thr Ala Ser Ser Pro Trp Thr Arg Ala 1170 1175 1180	4130
ggg ggc agc agg gga acg tct tct cat gct ccg tga tgc atg agg ctc Gly Gly Ser Arg Gly Thr Ser Ser His Ala Pro * Cys Met Arg Leu 1185 1190 1195	4178
tgc aca acc act aca cgc aga aga gcc tct ccc tgt ctc ccg gta aat Cys Thr Thr Thr Arg Arg Arg Ala Ser Pro Cys Leu Arg Val Asn 1200 1205 1210	4226
ga	4228

<210> 2
<211> 3463
<212> DNA

<213> Artificial Sequence

<220>

<223> fusion protein

<221> CDS

<222> (1)...(2193)

<221> CDS

<222> (2551)...(2595)

<221> CDS

<222> (2714)...(3043)

<221> CDS

<222> (3140)...(3463)

<400> 2

atg aat tta caa cca att ttc tgg att gga ctg atc agt tca gtt tgc	48
Met Asn Leu Gln Pro Ile Phe Trp Ile Gly Leu Ile Ser Ser Val Cys	
1 5 10 15	

tgt gtg ttt gct caa aca gat gaa aat aga tgt tta aaa gca aat gcc	96
Cys Val Phe Ala Gln Thr Asp Glu Asn Arg Cys Leu Lys Ala Asn Ala	
20 25 30	

aaa tca tgt gga gaa tgt ata caa gca ggg cca aat tgt ggg tgg tgc	144
Lys Ser Cys Gly Glu Cys Ile Gln Ala Gly Pro Asn Cys Gly Trp Cys	
35 40 45	

aca aat tca aca ttt tta cag gaa gga atg cct act tct gca cga tgt	192
Thr Asn Ser Thr Phe Leu Gln Glu Gly Met Pro Thr Ser Ala Arg Cys	
50 55 60	

gat gat tta gaa gcc tta aaa aag aag ggt tgc cct cca gat gac ata	240
Asp Asp Leu Glu Ala Leu Lys Lys Gly Cys Pro Pro Asp Asp Ile	
65 70 75 80	

gaa aat ccc aga ggc tcc aaa gat ata aag aaa aat aaa aat gta acc	288
Glu Asn Pro Arg Gly Ser Lys Asp Ile Lys Lys Asn Lys Asn Val Thr	
85 90 95	

aac cgt agc aaa gga aca gca gag aag ctc aag cca gag gat att cat	336
Asn Arg Ser Lys Gly Thr Ala Glu Lys Leu Lys Pro Glu Asp Ile His	
100 105 110	

cag atc caa cca cag cag ttg gtt ttg cga tta aga tca ggg gag cca	384
Gln Ile Gln Pro Gln Gln Leu Val Leu Arg Leu Arg Ser Gly Glu Pro	
115 120 125	

cag aca ttt aca tta aaa ttc aag aga gct gaa gac tat ccc att gac	432
Gln Thr Phe Thr Leu Lys Phe Lys Arg Ala Glu Asp Tyr Pro Ile Asp	
130 135 140	

ctc tac tac ctt atg gac ctg tct tat tca atg aaa gac gat ttg gag	480
Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Glu	
145 150 155 160	

aat gta aaa agt ctt gga aca gat ctg atg aat gaa atg agg agg att	528
Asn Val Lys Ser Leu Gly Thr Asp Leu Met Asn Glu Met Arg Arg Ile	
165 170 175	

act tcg gac ttc aga att gga ttt ggc tca ttt gtg gaa aag act gtg	576
Page 7	

1102-98.TXT

Thr	Ser	Asp	Phe	Arg	Ile	Gly	Phe	Gly	Ser	Phe	Val	Glu	Lys	Thr	Val	1102-98.TXT
180							185						190			
atg	cct	tac	att	agc	aca	aca	cca	gct	aag	ctc	agg	aac	cct	tgc	aca	624
Met	Pro	Tyr	Ile	Ser	Thr	Thr	Pro	Ala	Lys	Leu	Arg	Asn	Pro	Cys	Thr	
195							200						205			
agt	gaa	cag	aac	tgc	acc	acc	cca	ttt	agc	tac	aaa	aat	gtg	ctc	agt	672
Ser	Glu	Gln	Asn	Cys	Thr	Thr	Pro	Phe	Ser	Tyr	Lys	Asn	Val	Leu	Ser	
210							215						220			
ctt	act	aat	aaa	gga	gaa	gta	ttt	aat	gaa	ctt	gtt	gga	aaa	cag	cgc	720
Leu	Thr	Asn	Lys	Gly	Glu	Val	Phe	Asn	Glu	Leu	Val	Gly	Lys	Gln	Arg	
225							230						235			240
ata	tct	gga	aat	ttg	gat	tct	cca	gaa	ggt	ggt	ttc	gat	gcc	atc	atg	768
Ile	Ser	Gly	Asn	Leu	Asp	Ser	Pro	Glu	Gly	Gly	Phe	Asp	Ala	Ile	Met	
245							250						255			
caa	gtt	gca	gtt	tgt	gga	tca	ctg	att	ggc	tgg	agg	aat	gtt	aca	cgg	816
Gln	Val	Ala	Val	Cys	Gly	Ser	Leu	Ile	Gly	Trp	Arg	Asn	Val	Thr	Arg	
260							265						270			
ctg	ctg	gtg	ttt	tcc	aca	gat	gcc	ggg	ttt	cac	ttt	gct	gga	aat	ggg	864
Leu	Leu	Val	Phe	Ser	Thr	Asp	Ala	Gly	Phe	His	Phe	Ala	Gly	Asp	Gly	
275							280						285			
aaa	ctt	ggt	ggc	att	gtt	tta	cca	aat	gat	gga	caa	tgt	cac	ctg	gaa	912
Lys	Leu	Gly	Gly	Ile	Val	Leu	Pro	Asn	Asp	Gly	Gln	Cys	His	Leu	Glu	
290							295						300			
aat	aat	atg	tac	aca	atg	agc	cat	tat	tat	gat	tat	cct	tct	att	gct	960
Asn	Asn	Met	Tyr	Thr	Met	Ser	His	Tyr	Tyr	Asp	Tyr	Pro	Ser	Ile	Ala	
305							310						315			320
cac	ctt	gtc	cag	aaa	ctg	agt	gaa	aat	aat	att	cag	aca	att	ttt	gca	1008
His	Leu	Val	Gln	Lys	Leu	Ser	Glu	Asn	Asn	Ile	Gln	Thr	Ile	Phe	Ala	
325							330						335			
gtt	act	gaa	gaa	ttt	cag	cct	gtt	ta	aag	gag	ctg	aaa	aac	ttg	atc	1056
Val	Thr	Glu	Glu	Phe	Gln	Pro	Val	Tyr	Lys	Glu	Leu	Lys	Asn	Leu	Ile	
340							345						350			
cct	aag	tca	gca	gta	gga	aca	tta	tct	gca	aat	tct	agc	aat	gta	att	1104
Pro	Lys	Ser	Ala	Val	Gly	Thr	Leu	Ser	Ala	Asn	Ser	Ser	Asn	Val	Ile	
355							360						365			
cag	ttg	atc	att	gat	gca	tac	aat	tcc	ctt	tcc	tca	gaa	gtc	att	ttg	1152
Gln	Leu	Ile	Ile	Asp	Ala	Tyr	Asn	Ser	Leu	Ser	Ser	Glu	Val	Ile	Leu	
370							375						380			
gaa	aac	ggc	aaa	ttg	tca	gaa	gga	gta	aca	ata	agt	tac	aaa	tct	tac	1200
Glu	Asn	Gly	Lys	Leu	Ser	Glu	Gly	Val	Thr	Ile	Ser	Tyr	Lys	Ser	Tyr	
385							390						395			400
tgc	aag	aac	ggg	gtg	aat	gga	aca	ggg	gaa	aat	gga	aga	aaa	tgt	tcc	1248
Cys	Lys	Asn	Gly	Val	Asn	Gly	Thr	Gly	Glu	Asn	Gly	Arg	Lys	Cys	Ser	
405							410						415			
aat	att	tcc	att	gga	gat	gag	gtt	caa	ttt	gaa	att	agc	ata	act	tca	1296
Asn	Ile	Ser	Ile	Gly	Asp	Glu	Val	Gln	Phe	Glu	Ile	Ser	Ile	Thr	Ser	
420							425						430			

1102-98.TXT

aat aag tgt cca aaa aag gat tct gac agc ttt aaa att agg cct ctg	1344
Asn Lys Cys Pro Lys Lys Asp Ser Asp Ser Phe Lys Ile Arg Pro Leu	
435 440 445	
ggc ttt acg gag gaa gta gag gtt att ctt cag tac atc tgt gaa tgt	1392
Gly Phe Thr Glu Glu Val Glu Val Ile Leu Gln Tyr Ile Cys Glu Cys	
450 455 460	
gaa tgc caa agc gaa ggc atc cct gaa agt ccc aag tgt cat gaa gga	1440
Glu Cys Gln Ser Glu Gly Ile Pro Glu Ser Pro Lys Cys His Glu Gly	
465 470 475 480	
aat ggg aca ttt gag tgt ggc gcg tgc agg tgc aat gaa ggg cgt gtt	1488
Asn Gly Thr Phe Glu Cys Gly Ala Cys Arg Cys Asn Glu Gly Arg Val	
485 490 495	
ggt aga cat tgt gaa tgc agc aca gat gaa gtt aac agt gaa gac atg	1536
Gly Arg His Cys Glu Cys Ser Thr Asp Glu Val Asn Ser Glu Asp Met	
500 505 510	
gat gct tac tgc agg aaa gaa aac agt tca gaa atc tgc agt aac aat	1584
Asp Ala Tyr Cys Arg Lys Glu Asn Ser Ser Glu Ile Cys Ser Asn Asn	
515 520 525	
gga gag tgc gtc tgc gga cag tgt gtt tgt agg aag agg gat aat aca	1632
Gly Glu Cys Val Cys Gly Gln Cys Val Cys Arg Lys Arg Asp Asn Thr	
530 535 540	
aat gaa att tat tct ggc aaa ttc tgc gag tgt gat aat ttc aac tgt	1680
Asn Glu Ile Tyr Ser Gly Lys Phe Cys Glu Cys Asp Asn Phe Asn Cys	
545 550 555 560	
gat aga tcc aat ggc tta att tgt gga gga aat ggt gtt tgc aag tgt	1728
Asp Arg Ser Asn Gly Leu Ile Cys Gly Asn Gly Val Cys Lys Cys	
565 570 575	
cgt gtg tgt gag tgc aac ccc aac tac act ggc agt gca tgt gac tgt	1776
Arg Val Cys Glu Cys Asn Pro Asn Tyr Thr Gly Ser Ala Cys Asp Cys	
580 585 590	
tct ttg gat act agt act tgt gaa gcc agc aac gga cag atc tgc aat	1824
Ser Leu Asp Thr Ser Thr Cys Glu Ala Ser Asn Gly Gln Ile Cys Asn	
595 600 605	
ggc cgg ggc atc tgc gag tgt ggt gtc tgt aag tgt aca gat ccg aag	1872
Gly Arg Gly Ile Cys Glu Cys Gly Val Cys Lys Cys Thr Asp Pro Lys	
610 615 620 620	
ttt caa ggg caa acg tgt gag atg tgt cag acc tgc ctt ggt gtc tgt	1920
Phe Gln Gly Gln Thr Cys Glu Met Cys Gln Thr Cys Leu Gly Val Cys	
625 630 635 640	
gct gag cat aaa gaa tgt gtt cag tgc aga gcc ttc aat aaa gga gaa	1968
Ala Glu His Lys Glu Cys Val Gln Cys Arg Ala Phe Asn Lys Gly Glu	
645 650 655	
aag aaa gac aca tgc aca cag gaa tgt tcc tat ttt aac att acc aag	2016
Lys Lys Asp Thr Cys Thr Gln Glu Cys Ser Tyr Phe Asn Ile Thr Lys	
660 665 670	
gta gaa agt cgg gac aaa tta ccc cag ccg gtc caa cct gat cct gtg	2064
Val Glu Ser Arg Asp Lys Leu Pro Gln Pro Val Gln Pro Asp Pro Val	
675 680 685	

1102-98.TXT

tcc cat tgt aag gag aag gat gtt gac gac tgt tgg ttc tat ttt acg	2112
Ser His Cys Lys Glu Lys Asp Val Asp Asp Cys Trp Phe Tyr Phe Thr	
690 695 700	
tat tca gtg aat ggg aac aac gag gtc atg gtt cat gtt gtg gag aat	2160
Tyr Ser Val Asn Gly Asn Asn Glu Val Met Val His Val Val Glu Asn	
705 710 715 720	
cca gag tgt ccc act ggt cca gag gat ccc gag ctgcttggaa caggctcagc	2213
Pro Glu Cys Pro Thr Gly Pro Glu Asp Pro Glu	
725 730	
gctccgtcct ggacgcattcc cggctatgca gccccagttcc agggcagcaa ggcaggcccc	2273
gtctgcctct tcaccccgag cctctgccc ccccactcat gctcagggag agggtcttct	2333
ggctttttcc caggctctgg gcagggcacag gcttaggtgcc ccttaaccctcg gcccgtcaca	2393
caaaggggca ggtgctgggc tcagacactc caagagccat atccgggagg accctgcccc	2453
tgacctaagc ccaccccaa ggcacaaactc tccactccct cagctcggac accttctctc	2513
ctccagatt ccagtaactc ccaatcttct ctctgca gag ccc aaa tct tgt gac	2568
Glu Pro Lys Ser Cys Asp	
735	
aaa act cac aca tgc cca ccg tgc cca ggtaagccag cccaggccctc	2615
Lys Thr His Thr Cys Pro Pro Cys Pro	
740 745	
gccctccagc tcaaggcggg acaggtgccc tagagtaggcc tgcattccagg gacaggcccc	2675
agccgggtgc tgacacgtcc acctccatct cttcctca gca cct gaa ctc ctg ggg	2731
Ala Pro Glu Leu Leu Gly	
750	
gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg	2779
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met	
755 760 765	
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtg agc cac	2827
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His	
770 775 780	
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg	2875
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val	
785 790 795 800	
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac	2923
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr	
805 810 815	
cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc	2971
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly	
820 825 830	
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc	3019
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile	
835 840 845	
gag aaa acc atc tcc aaa gcc aaa ggtgggaccc gtggggtgcg agggccacat	3073
Glu Lys Thr Ile Ser Lys Ala Lys	
850 855	
ggacagaggc cggctcgccc caccctctgc cctgagagt accgctgtac caacctctgt	3133
cctaca ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc	3181
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser	
860 865 870	

1102-98.TXT

ccg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa	3229
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys	
875 880 885	
ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag	3277
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln	
890 895 900	
ccg gag aac aac tac aag acc acg cct ccc gtg ctg gat tcc gac ggc	3325
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly	
905 910 915	
tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag	3373
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln	
920 925 930	
cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac	3421
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn	
935 940 945 950	
cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga	3463
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys *	
955 960	

<210> 3

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide linear

<400> 3

Cys Leu His Gly Pro Glu Ile Leu Asp Val Pro Ser Thr
1 5 10

<210> 4

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA oligonucleotide

<400> 4

gcggatcccg agctgctgga agcaggctca g

31

<210> 5

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA oligonucleotide

<400> 5

cctctagacg gccgtcgac ac tcattta

27

<210> 6

1102-98.TXT

<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic DNA oligonucleotide

<400> 6
ctagaccacc atgttcccca ccgagagcgc atggcttggg aagcgaggcg cgaaccggg 60
ccccggagct gca 73

<210> 7
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic DNA oligonucleotide

<400> 7
gcttcggggc ccgggttcgc gcctcgcttc ccaagccatg cgctctcggt gggaaacatg 60
gtggt 65

<210> 8
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic DNA oligonucleotide

<400> 8
ctccggaga cggtgatgct gttgctgtgc ctgggggtcc cgaccggcag g 51

<210> 9
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic DNA oligonucleotide

<400> 9
cctgcggtc gggaccccca ggcacagcaa cagcatcacc gtctcccgga gtcga 55

<210> 10
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic DNA oligonucleotide

<400> 10
cactgcaggc aggccttaca acgtggacac tgagagc 37

<210> 11
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic DNA oligonucleotide

1102-98.TXT

<400> 11	
gcagaaacct gtaaaatcagc ag	22
<210> 12	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> synthetic DNA oligonucleotide	
<400> 12	
gcatttatgc ggaaagatgt gc	22
<210> 13	
<211> 29	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> synthetic DNA oligonucleotide	
<400> 13	
cgggatccgt gaaataacgt ttgggtctt	29
<210> 14	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> synthetic DNA oligonucleotide	
<400> 14	
gcggaaaaga tgaatttaca ac	22
<210> 15	
<211> 27	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> synthetic DNA oligonucleotide	
<400> 15	
gtgggatcct ctggaccagt gggacac	27
<210> 16	
<211> 10	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> synthetic peptide linear	
<400> 16	
Gly Pro Glu Ile Leu Asp Val Pro Ser Thr	
1 5 10	
<210> 17	
<211> 10	

<212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic peptide linear

<400> 17
 Gly Pro Glu Ile Leu Glu Val Pro Ser Thr
 1 5 10

<210> 18
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic peptide linear

<400> 18
 Gly Arg Gly Asp Ser Pro
 1 5

<210> 19
 <211> 4675
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence encoding fusion protein

<221> CDS
 <222> (1)...(3405)

<221> CDS
 <222> (3763)...(3807)

<221> CDS
 <222> (3926)...(4255)

<221> CDS
 <222> (4352)...(4675)

<400> 19
 atg ggg cca gaa cgg aca ggg gcc gcg ccg ctg ccg ctg ctg ctg gtg 48
 Met Gly Pro Glu Arg Thr Gly Ala Ala Pro Leu Pro Leu Leu Leu Val
 1 5 10 15

tta gcg ctc agt caa ggc att tta aat tgt tgt ttg gcc tac aat gtt 96
 Leu Ala Leu Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val
 20 25 30

ggt ctc cca gaa gca aaa ata ttt tcc ggt cct tca agt gaa cag ttt 144
 Gly Leu Pro Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe
 35 40 45

ggg tat gca gtg cag cag ttt ata aat cca aaa ggc aac tgg tta ctg 192
 Gly Tyr Ala Val Gln Gln Phe Ile Asn Pro Lys Gly Asn Trp Leu Leu
 50 55 60

gtt ggt tca ccc tgg agt ggc ttt cct gag aac cga atg gga gat gtg 240
 Val Gly Ser Pro Trp Ser Gly Phe Pro Glu Asn Arg Met Gly Asp Val

1102-98.TXT

65	70	75	80	
tat aaa tgt cct gtt gac cta tcc act gcc aca tgt gaa aaa cta aat				288
Tyr Lys Cys Pro Val Asp Leu Ser Thr Ala Thr Cys Glu Lys Leu Asn				
85	90	95		
ttg caa act tca aca agc att cca aat gtt act gag atg aaa acc aac				336
Leu Gln Thr Ser Thr Ser Ile Pro Asn Val Thr Glu Met Lys Thr Asn				
100	105	110		
atg agc ctc ggc ttg atc ctc acc agg aac atg gga act gga ggt ttt				384
Met Ser Leu Gly Leu Ile Leu Thr Arg Asn Met Gly Thr Gly Gly Phe				
115	120	125		
ctc aca tgt ggt cct ctg tgg gca cag caa tgt ggg aat cag tat tac				432
Leu Thr Cys Gly Pro Leu Trp Ala Gln Gln Cys Gly Asn Gln Tyr Tyr				
130	135	140		
aca acg ggt gtg tgt tct gac atc agt cct gat ttt cag ctc tca gcc				480
Thr Thr Gly Val Cys Ser Asp Ile Ser Pro Asp Phe Gln Leu Ser Ala				
145	150	155	160	
agc ttc tca cct gca act cag ccc tgc cct tcc ctc ata gat gtt gtg				528
Ser Phe Ser Pro Ala Thr Gln Pro Cys Pro Ser Leu Ile Asp Val Val				
165	170	175		
gtt gtg tgt gat gaa tca aat agt att tat cct tgg gat gca gta aag				576
Val Val Cys Asp Glu Ser Asn Ser Ile Tyr Pro Trp Asp Ala Val Lys				
180	185	190		
aat ttt ttg gaa aaa ttt gta caa ggc ctt gat ata ggc ccc aca aag				624
Asn Phe Leu Glu Lys Phe Val Gln Gly Leu Asp Ile Gly Pro Thr Lys				
195	200	205		
aca cag gtg ggg tta att cag tat gcc aat aat cca aga gtt gtg ttt				672
Thr Gln Val Gly Leu Ile Gln Tyr Ala Asn Asn Pro Arg Val Val Phe				
210	215	220		
aac ttg aac aca tat aaa acc aaa gaa gaa atg att gta gca aca tcc				720
Asn Leu Asn Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser				
225	230	235	240	
cag aca tcc caa tat ggt ggg gac ctc aca aac aca ttc gga gca att				768
Gln Thr Ser Gln Tyr Gly Asp Leu Thr Asn Thr Phe Gly Ala Ile				
245	250	255		
caa tat gca aga aaa tat gcc tat tca gca gct tct ggt ggg cga cga				816
Gln Tyr Ala Arg Lys Tyr Ala Tyr Ser Ala Ala Ser Gly Gly Arg Arg				
260	265	270		
agt gct acg aaa gta atg gta gtt gta act gac ggt gaa tca cat gat				864
Ser Ala Thr Lys Val Met Val Val Thr Asp Gly Glu Ser His Asp				
275	280	285		
ggt tca atg ttg aaa gct gtg att gat caa tgc aac cat gac aat ata				912
Gly Ser Met Leu Lys Ala Val Ile Asp Gln Cys Asn His Asp Asn Ile				
290	295	300		
ctg agg ttt ggc ata gca gtt ctt ggg tac tta aac aga aac gcc ctt				960
Leu Arg Phe Gly Ile Ala Val Leu Gly Tyr Leu Asn Arg Asn Ala Leu				
305	310	315	320	
gat act aaa aat tta ata aaa gaa ata aaa gcg atc gct agt att cca				1008

1102-98.TXT

Asp	Thr	Lys	Asn	Leu	Ile	Lys	Glu	Ile	Lys	Ala	Ile	Ala	Ser	Ile	Pro		
325						330				335							
aca	gaa	aga	ta	ttt	ttc	aat	gtg	tct	gat	gaa	gca	gct	cta	cta	gaa	1056	
Thr	Glu	Arg	Tyr	Phe	Phe	Asn	Val	Ser	Asp	Glu	Ala	Ala	Leu	Leu	Glu		
340				345									350				
aag	gct	ggg	aca	tta	gga	gaa	caa	att	ttc	agc	att	gaa	ggt	act	gtt	1104	
Lys	Ala	Gly	Thr	Leu	Gly	Glu	Gln	Ile	Phe	Ser	Ile	Glu	Gly	Thr	Val		
355				360								365					
caa	gga	gga	gac	aac	ttt	cag	atg	gaa	atg	tca	caa	gtg	gga	ttc	agt	1152	
Gln	Gly	Gly	Asp	Asn	Phe	Gln	Met	Glu	Met	Ser	Gln	Val	Gly	Phe	Ser		
370				375							380						
gca	gat	ta	c	tct	tct	caa	aat	gat	att	ctg	atg	ctg	ggt	gca	gtg	gga	1200
Ala	Asp	Tyr	Ser	Ser	Gln	Asn	Asp	Ile	Leu	Met	Leu	Gly	Ala	Val	Gly		
385				390						395				400			
gct	ttt	ggc	tgg	agt	ggg	acc	att	gtc	cag	aag	aca	tct	cat	ggc	cat	1248	
Ala	Phe	Gly	Trp	Ser	Gly	Thr	Ile	Val	Gln	Lys	Thr	Ser	His	Gly	His		
405									410				415				
ttg	atc	ttt	cct	aaa	caa	gcc	ttt	gac	caa	att	ctg	cag	gac	aga	aat	1296	
Leu	Ile	Phe	Pro	Lys	Gln	Ala	Phe	Asp	Gln	Ile	Leu	Gln	Asp	Arg	Asn		
420								425					430				
cac	agt	tca	tat	tta	ggt	ta	c	tct	gtg	gct	gca	att	tct	act	gga	gaa	1344
His	Ser	Ser	Tyr	Leu	Gly	Tyr	Ser	Val	Ala	Ala	Ile	Ser	Thr	Gly	Glu		
435								440					445				
agc	act	cac	ttt	gtt	gct	ggt	gct	cct	cg	gca	aat	tat	acc	ggc	cag	1392	
Ser	Thr	His	Phe	Val	Ala	Gly	Ala	Pro	Arg	Ala	Asn	Tyr	Thr	Gly	Gln		
450						455					460						
ata	gtg	cta	tat	agt	gtg	aat	gag	aat	ggc	aat	atc	acg	gtt	att	cag	1440	
Ile	Val	Leu	Tyr	Ser	Val	Asn	Glu	Asn	Gly	Asn	Ile	Thr	Val	Ile	Gln		
465						470					475				480		
gct	cac	cga	ggt	gac	cag	att	ggc	tcc	tat	ttt	ggt	agt	gtg	ctg	tgt	1488	
Ala	His	Arg	Gly	Asp	Gln	Ile	Gly	Ser	Tyr	Phe	Gly	Ser	Val	Leu	Cys		
485								490						495			
tca	gtt	gat	gtg	gat	aaa	gac	acc	att	aca	gac	gtg	ctc	ttg	gta	ggt	1536	
Ser	Val	Asp	Val	Asp	Lys	Asp	Thr	Ile	Thr	Asp	Val	Leu	Leu	Val	Gly		
500								505					510				
gca	cca	atg	ta	atg	agt	gac	cta	aag	aaa	gag	gaa	gga	aga	gtc	ta	1584	
Ala	Pro	Met	Tyr	Met	Ser	Asp	Leu	Lys	Lys	Glu	Glu	Gly	Arg	Val	Tyr		
515							520					525					
ctg	ttt	act	atc	aaa	aag	ggc	att	ttg	ggt	cag	cac	caa	ttt	ctt	gaa	1632	
Leu	Phe	Thr	Ile	Lys	Lys	Gly	Ile	Leu	Gly	Gln	His	Gln	Phe	Leu	Glu		
530						535					540						
ggc	ccc	gag	ggc	att	gaa	aac	act	cga	ttt	ggt	tca	gca	att	gca	gct	1680	
Gly	Pro	Glu	Gly	Ile	Glu	Asn	Thr	Arg	Phe	Gly	Ser	Ala	Ile	Ala	Ala		
545						550					555				560		
ctt	tca	gac	atc	aac	atg	gat	ggc	ttt	aat	gat	gtg	att	gtt	ggt	tca	1728	
Leu	Ser	Asp	Ile	Asn	Met	Asp	Gly	Phe	Asn	Asp	Val	Ile	Val	Gly	Ser		
565								570					575				

1102-98.TXT

cca cta gaa aat cag aat tct gga gct gta tac att tac aat ggt cat	1776
Pro Leu Glu Asn Gln Asn Ser Gly Ala Val Tyr Ile Tyr Asn Gly His	
580 585 590	
cag ggc act atc cgc aca aag tat tcc cag aaa atc ttg gga tcc gat	1824
Gln Gly Thr Ile Arg Thr Lys Tyr Ser Gln Lys Ile Leu Gly Ser Asp	
595 600 605	
gga gcc ttt agg agc cat ctc cag tac ttt ggg agg tcc ttg gat ggc	1872
Gly Ala Phe Arg Ser His Leu Gln Tyr Phe Gly Arg Ser Leu Asp Gly	
610 615 620	
tat gga gat tta aat ggg gat tcc atc acc gat gtg tct att ggt gcc	1920
Tyr Gly Asp Leu Asn Gly Asp Ser Ile Thr Asp Val Ser Ile Gly Ala	
625 630 635 640	
ttt gga caa gtg gtt caa ctc tgg tca caa agt att gct gat gta gct	1968
Phe Gly Gln Val Val Gln Leu Trp Ser Gln Ser Ile Ala Asp Val Ala	
645 650 655	
ata gaa gct tca ttc aca cca gaa aaa atc act ttg gtc aac aag aat	2016
Ile Glu Ala Ser Phe Thr Pro Glu Lys Ile Thr Leu Val Asn Lys Asn	
660 665 670	
gct cag ata att ctc aaa ctc tgc ttc agt gca aag ttc aga cct act	2064
Ala Gln Ile Ile Leu Lys Leu Cys Phe Ser Ala Lys Phe Arg Pro Thr	
675 680 685	
aag caa aac aat caa gtg gcc att gta tat aac atc aca ctt gat gca	2112
Lys Gln Asn Asn Gln Val Ala Ile Val Tyr Asn Ile Thr Leu Asp Ala	
690 695 700	
gat gga ttt tca tcc aga gta acc tcc agg ggg tta ttt aaa gaa aac	2160
Asp Gly Phe Ser Ser Arg Val Thr Ser Arg Gly Leu Phe Lys Glu Asn	
705 710 715 720	
aat gaa agg tgc ctg cag aag aat atg gta gta aat caa gca cag agt	2208
Asn Glu Arg Cys Leu Gln Lys Asn Met Val Val Asn Gln Ala Gln Ser	
725 730 735	
tgc ccc gag cac atc att tat ata cag gag ccc tct gat gtt gtc aac	2256
Cys Pro Glu His Ile Ile Tyr Ile Gln Glu Pro Ser Asp Val Val Asn	
740 745 750	
tct ttg gat ttg cgt gtg gac atc agt ctg gaa aac cct ggc act agc	2304
Ser Leu Asp Leu Arg Val Asp Ile Ser Leu Glu Asn Pro Gly Thr Ser	
755 760 765	
cct gcc ctt gaa gcc tat tct gag act gcc aag gtc ttc agt att cct	2352
Pro Ala Leu Glu Ala Tyr Ser Glu Thr Ala Lys Val Phe Ser Ile Pro	
770 775 780	
ttc cac aaa gac tgt ggt gag gat gga ctt tgc att tct gat cta gtc	2400
Phe His Lys Asp Cys Gly Glu Asp Gly Leu Cys Ile Ser Asp Leu Val	
785 790 795 800	
cta gat gtc cga caa ata cca gct gct caa gaa caa ccc ttt att gtc	2448
Leu Asp Val Arg Gln Ile Pro Ala Ala Gln Glu Gln Pro Phe Ile Val	
805 810 815	
agc aac caa aac aaa agg tta aca ttt tca gta aca ctg aaa aat aaa	2496
Ser Asn Gln Asn Lys Arg Leu Thr Phe Ser Val Thr Leu Lys Asn Lys	
820 825 830	

1102-98.TXT

agg gaa agt gca tac aac act gga att gtt gtt gat ttt tca gaa aac	2544
Arg Glu Ser Ala Tyr Asn Thr Gly Ile Val Val Asp Phe Ser Glu Asn	
835 840 845	
ttg ttt ttt gca tca ttc tcc cta ccg gtt gat ggg aca gaa gta aca	2592
Leu Phe Phe Ala Ser Phe Ser Leu Pro Val Asp Gly Thr Glu Val Thr	
850 855 860	
tgc cag gtg gct gca tct cag aag tct gtt gcc tgc gat gta ggc tac	2640
Cys Gln Val Ala Ala Ser Gln Lys Ser Val Ala Cys Asp Val Gly Tyr	
865 870 875 880	
cct gct tta aag aga gaa caa cag gtg act ttt act att aac ttt gac	2688
Pro Ala Leu Lys Arg Glu Gln Gln Val Thr Phe Thr Ile Asn Phe Asp	
885 890 895	
ttc aat ctt caa aac ctt cag aat cag gcg tct ctc agt ttc caa gcc	2736
Phe Asn Leu Gln Asn Leu Gln Asn Gln Ala Ser Leu Ser Phe Gln Ala	
900 905 910	
tta agt gaa agc caa gaa gaa aac aag gct gat aat ttg gtc aac ctc	2784
Leu Ser Glu Ser Gln Glu Glu Asn Lys Ala Asp Asn Leu Val Asn Leu	
915 920 925	
aaa att cct ctc ctg tat gat gct gaa att cac tta aca aga tct acc	2832
Lys Ile Pro Leu Leu Tyr Asp Ala Glu Ile His Leu Thr Arg Ser Thr	
930 935 940	
aac ata aat ttt tat gaa atc tct tcg gat ggg aat gtt cct tca atc	2880
Asn Ile Asn Phe Tyr Glu Ile Ser Ser Asp Gly Asn Val Pro Ser Ile	
945 950 955 960	
gtg cac agt ttt gaa gat gtt ggt cca aaa ttc atc ttc tcc ctg aag	2928
Val His Ser Phe Glu Asp Val Gly Pro Lys Phe Ile Phe Ser Leu Lys	
965 970 975	
gta aca aca gga agt gtt cca gta agc atg gca act gta atc atc cac	2976
Val Thr Thr Gly Ser Val Pro Val Ser Met Ala Thr Val Ile Ile His	
980 985 990	
atc cct cag tat acc aaa gaa aag aac cca ctg atg tac cta act ggg	3024
Ile Pro Gln Tyr Thr Lys Glu Lys Asn Pro Leu Met Tyr Leu Thr Gly	
995 1000 1005	
gtg caa aca gac aag gct ggt gac atc agt tgt aat gca gat atc aat	3072
Val Gln Thr Asp Lys Ala Gly Asp Ile Ser Cys Asn Ala Asp Ile Asn	
1010 1015 1020	
cca ctg aaa ata gga caa aca tct tct gta tct ttc aaa agt gaa	3120
Pro Leu Lys Ile Gly Gln Thr Ser Ser Val Ser Phe Lys Ser Glu	
1025 1030 1035 1040	
aat ttc agg cac acc aaa gaa ttg aac tgc aga act gct tcc tgt agt	3168
Asn Phe Arg His Thr Lys Glu Leu Asn Cys Arg Thr Ala Ser Cys Ser	
1045 1050 1055	
aat gtt acc tgc tgg ttg aaa gac gtt cac atg aaa gga gaa tac ttt	3216
Asn Val Thr Cys Trp Leu Lys Asp Val His Met Lys Gly Glu Tyr Phe	
1060 1065 1070	
gtt aat gtg act acc aga att tgg aac ggg act ttc gca tca tca acg	3264
Val Asn Val Thr Thr Arg Ile Trp Asn Gly Thr Phe Ala Ser Ser Thr	

1102-98.TXT

1075	1080	1085	
ttc cag aca gta cag cta acg gca gct gca gaa atc aac acc tat aac Phe Gln Thr Val Gln Leu Thr Ala Ala Ala Glu Ile Asn Thr Tyr Asn 1090	1095	1100	3312
cct gag ata tat gtg att gaa gat aac act gtt acg att ccc ctg atg Pro Glu Ile Tyr Val Ile Glu Asp Asn Thr Val Thr Ile Pro Leu Met 1105	1110	1115	3360
ata atg aaa cct gat gag aaa gcc gaa gta cca aca gat ccc gag Ile Met Lys Pro Asp Glu Lys Ala Glu Val Pro Thr Asp Pro Glu 1125	1130	1135	3405
ctgcttggaaag caggctcagc gctcctgcct ggacgcattcc cggctatgca gccccagtc 3465 agggcagcaa ggcaggcccc gtctgcctct tcacccggag cctctgccc ccccaactcat 3525 gctcaggagg agggtcttct ggcttttcc caggctctgg gcaggcacag gctagggtgcc 3585 cctaaccagg gcccgcaca caaaggggca ggtgctggc tcagacctgc caagagccat 3645 atccgggagg accctgcccc tgacctaagc ccacccaaa ggccaaactc tccactccct 3705 cagctcggac accttctctc ctccagatt ccagtaactc ccaatcttct ctctgca gag 3765 Glu			
ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro 1140	1145	1150	3807
ggtaagccag cccaggcctc gcccctccagc tcaaggcggg acaggtgccc tagatgtcc 3867 tgcatccagg gacaggcccc agccgggtgc tgacacgtcc acctccatct cttcctca 3925 gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa 3973 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys 1155	1160	1165	
ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val 1170	1175	1180	4021
gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr 1185	1190	1195	4069
gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg ccg gag gag Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu 1200	1205	1210	4117
cag tac aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His 1215	1220	1225	4165
cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys 1235	1240	1245	4213
gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys 1250	1255	1260	4255
ggggggaccc gtgggggtgcg agggccacat ggacagagggc cggctcgcc caccctctgc 4315 cctgagatg accgctgtac caaccctctgt cctaca ggg cag ccc cga gaa cca 4369 Gly Gln Pro Arg Glu Pro 1265			
cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag Page 19			4417

1102-98.TXT

Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	
1270								1275					1280			
gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	4465
Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	
1285						1290					1295					
gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	4513
Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	
1300						1305					1310					
cct	ccc	gtg	ctg	gat	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	4561
Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	
1315						1320					1325				1330	
acc	gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	4609
Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	
1335						1340					1345					
gtg	atg	cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	4657
Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	
1350						1355					1360					
ctg	tct	ccg	ggt	aaa	tga											4675
Leu	Ser	Pro	Gly	Lys	*											
1365																

<210> 20
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic DNA oligonucleotide

<400> 20
gctcgagcaa acccagcgca actacgg 27

<210> 21
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic DNA oligonucleotide

<400> 21
atagtgcctt gatgaccatt g 21

<210> 22
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic DNA oligonucleotide

<400> 22
gatggcttta atgatgtgat tg 22

<210> 23
<211> 21

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic DNA oligonucleotide

<400> 23
tgttggtaact tcggctttct c

21

<210> 24
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide circular

<400> 24
Cys Ile Pro Glu Leu Ile Val Cys
1 5

<210> 25
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide circular

<400> 25
Cys Met Arg Tyr Thr Ser Ala Cys
1 5

<210> 26
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide circular

<400> 26
Cys Glu Trp Met Lys Arg Phe Cys
1 5

<210> 27
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide circular

<400> 27
Cys Tyr Thr Thr Arg Leu Lys Cys
1 5

<210> 28
<211> 8

1102-98.TXT

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide circular

<400> 28
Cys Leu Arg Tyr Ser Val Pro Cys
1 5

<210> 29
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide circular

<400> 29
Cys Ile Val Asn Arg Leu Gly Cys
1 5

<210> 30
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide circular

<400> 30
Cys Gly Leu Gln Ala Leu Pro Cys
1 5

<210> 31
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide circular

<400> 31
Cys Lys Leu Lys Gly Thr Met Cys
1 5

<210> 32
<211> 1218
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 32
Met Phe Pro Thr Glu Ser Ala Trp Leu Gly Lys Arg Gly Ala Asn Pro
1 5 10 15
Gly Pro Glu Ala Ala Leu Arg Glu Thr Val Met Leu Leu Leu Cys Leu
20 25 30

1102-98.TXT

Gly Val Pro Thr Gly Arg Pro Tyr Asn Val Asp Thr Glu Ser Ala Leu
 35 40 45
 Leu Tyr Gln Gly Pro His Asn Thr Leu Phe Gly Tyr Ser Val Val Leu
 50 55 60
 His Ser His Gly Ala Asn Arg Trp Leu Leu Val Gly Ala Pro Thr Ala
 65 70 75 80
 Asn Trp Leu Ala Asn Ala Ser Val Ile Asn Pro Gly Ala Ile Tyr Arg
 85 90 95
 Cys Arg Ile Gly Lys Asn Pro Gly Gln Thr Cys Glu Gln Leu Gln Leu
 100 105 110
 Gly Ser Pro Asn Gly Glu Pro Cys Gly Lys Thr Cys Leu Glu Glu Arg
 115 120 125
 Asp Asn Gln Trp Leu Gly Val Thr Leu Ser Arg Gln Pro Gly Glu Asn
 130 135 140
 Gly Ser Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile
 145 150 155 160
 Lys Asn Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro
 165 170 175
 Asp Leu Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Cys Tyr Gln Asp
 180 185 190
 Tyr Val Lys Lys Phe Gly Glu Asn Phe Ala Ser Cys Gln Ala Gly Ile
 195 200 205
 Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro Gly Ser
 210 215 220
 Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Asn Ile Thr Thr Asn Lys
 225 230 235 240
 Tyr Lys Ala Phe Leu Asp Lys Gln Asn Gln Val Lys Phe Gly Ser Tyr
 245 250 255
 Leu Gly Tyr Ser Val Gly Ala Gly His Phe Arg Ser Gln His Thr Thr
 260 265 270
 Glu Val Val Gly Gly Ala Pro Gln His Glu Gln Ile Gly Lys Ala Tyr
 275 280 285
 Ile Phe Ser Ile Asp Glu Lys Glu Leu Asn Ile Leu His Glu Met Lys
 290 295 300
 Gly Lys Lys Leu Gly Ser Tyr Phe Gly Ala Ser Val Cys Ala Val Asp
 305 310 315 320
 Leu Asn Ala Asp Gly Phe Ser Asp Leu Leu Val Gly Ala Pro Met Gln
 325 330 335
 Ser Thr Ile Arg Glu Glu Gly Arg Val Phe Val Tyr Ile Asn Ser Gly
 340 345 350
 Ser Gly Ala Val Met Asn Ala Met Glu Thr Asn Leu Val Gly Ser Asp
 355 360 365
 Lys Tyr Ala Ala Arg Phe Gly Glu Ser Ile Val Asn Leu Gly Asp Ile
 370 375 380
 Asp Asn Asp Gly Phe Glu Asp Val Ala Ile Gly Ala Pro Gln Glu Asp
 385 390 395 400
 Asp Leu Gln Gly Ala Ile Tyr Ile Tyr Asn Gly Arg Ala Asp Gly Ile
 405 410 415
 Ser Ser Thr Phe Ser Gln Arg Ile Glu Gly Leu Gln Ile Ser Lys Ser
 420 425 430
 Leu Ser Met Phe Gly Gln Ser Ile Ser Gly Gln Ile Asp Ala Asp Asn
 435 440 445
 Asn Gly Tyr Val Asp Val Ala Val Gly Ala Phe Arg Ser Asp Ser Ala
 450 455 460
 Val Leu Leu Arg Thr Arg Pro Val Val Ile Val Asp Ala Ser Leu Ser
 465 470 475 480
 His Pro Glu Ser Val Asn Arg Thr Lys Phe Asp Cys Val Glu Asn Gly
 485 490 495
 Trp Pro Ser Val Cys Ile Asp Leu Thr Leu Cys Phe Ser Tyr Lys Gly
 500 505 510
 Lys Glu Val Pro Gly Tyr Ile Val Leu Phe Tyr Asn Met Ser Leu Asp
 515 520 525
 Val Asn Arg Lys Ala Glu Ser Pro Pro Arg Phe Tyr Phe Ser Ser Asn

1102-98.TXT

530	535	540													
Gly	Thr	Ser	Asp	Val	Ile	Thr	Gly	Ser	Ile	Gln	Val	Ser	Ser	Arg	Glu
545	550	555	560												
Ala	Asn	Cys	Arg	Thr	His	Gln	Ala	Phe	Met	Arg	Lys	Asp	Val	Arg	Asp
565	570	575													
Ile	Leu	Thr	Pro	Ile	Gln	Ile	Glu	Ala	Ala	Tyr	His	Leu	Gly	Pro	His
580	585	590													
Val	Ile	Ser	Lys	Arg	Ser	Thr	Glu	Glu	Phe	Pro	Pro	Leu	Gln	Pro	Ile
595	600	605													
Leu	Gln	Gln	Lys	Lys	Glu	Lys	Asp	Ile	Met	Lys	Lys	Thr	Ile	Asn	Phe
610	615	620													
Ala	Arg	Phe	Cys	Ala	His	Glu	Asn	Cys	Ser	Ala	Asp	Leu	Gln	Val	Ser
625	630	635	640												
Ala	Lys	Ile	Gly	Phe	Leu	Lys	Pro	His	Glu	Asn	Lys	Thr	Tyr	Leu	Ala
645	650	655													
Val	Gly	Ser	Met	Lys	Thr	Leu	Met	Leu	Asn	Val	Ser	Leu	Phe	Asn	Ala
660	665	670													
Gly	Asp	Asp	Ala	Tyr	Glu	Thr	Leu	His	Val	Lys	Leu	Pro	Val	Gly	
675	680	685													
Leu	Tyr	Phe	Ile	Lys	Ile	Leu	Glu	Leu	Glu	Lys	Gln	Ile	Asn	Cys	
690	695	700													
Glu	Val	Thr	Asp	Asn	Ser	Gly	Val	Val	Gln	Leu	Asp	Cys	Ser	Ile	Gly
705	710	715	720												
Tyr	Ile	Tyr	Val	Asp	His	Leu	Ser	Arg	Ile	Asp	Ile	Ser	Phe	Leu	Leu
725	730	735													
Asp	Val	Ser	Ser	Leu	Ser	Arg	Ala	Glu	Glu	Asp	Leu	Ser	Ile	Thr	Val
740	745	750													
His	Ala	Thr	Cys	Glu	Asn	Glu	Glu	Glu	Met	Asp	Asn	Leu	Lys	His	Ser
755	760	765													
Arg	Val	Thr	Val	Ala	Ile	Pro	Leu	Lys	Tyr	Glu	Val	Lys	Leu	Thr	Val
770	775	780													
His	Gly	Phe	Val	Asn	Pro	Thr	Ser	Phe	Val	Tyr	Gly	Ser	Asn	Asp	Glu
785	790	795	800												
Asn	Glu	Pro	Glu	Thr	Cys	Met	Val	Glu	Lys	Met	Asn	Leu	Thr	Phe	His
805	810	815													
Val	Ile	Asn	Thr	Gly	Asn	Ser	Met	Ala	Pro	Asn	Val	Ser	Val	Glu	Ile
820	825	830													
Met	Val	Pro	Asn	Ser	Phe	Ser	Pro	Gln	Thr	Asp	Lys	Leu	Phe	Asn	Ile
835	840	845													
Leu	Asp	Val	Gln	Thr	Thr	Gly	Glu	Cys	His	Phe	Glu	Asn	Tyr	Gln	
850	855	860													
Arg	Val	Cys	Ala	Leu	Glu	Gln	Lys	Ser	Ala	Met	Gln	Thr	Leu	Lys	
865	870	875	880												
Gly	Ile	Val	Arg	Phe	Leu	Ser	Lys	Thr	Asp	Lys	Arg	Leu	Leu	Tyr	Cys
885	890	895													
Ile	Lys	Ala	Asp	Pro	His	Cys	Leu	Asn	Phe	Leu	Cys	Asn	Phe	Gly	Lys
900	905	910													
Met	Glu	Ser	Gly	Lys	Glu	Ala	Ser	Val	His	Ile	Gln	Leu	Glu	Gly	Arg
915	920	925													
Pro	Ser	Ile	Leu	Glu	Met	Asp	Glu	Thr	Ser	Ala	Leu	Lys	Phe	Glu	Ile
930	935	940													
Arg	Ala	Thr	Gly	Phe	Pro	Glu	Pro	Asn	Pro	Arg	Val	Ile	Glu	Leu	Asn
945	950	955	960												
Lys	Asp	Glu	Asn	Val	Ala	His	Val	Leu	Leu	Glu	Gly	Leu	His	His	Gln
965	970	975													
Arg	Pro	Lys	Arg	Tyr	Phe	Thr	Asp	Pro	Glu	Glu	Pro	Lys	Ser	Cys	Asp
980	985	990													
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly
995	1000	1005													
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile
1010	1015	1020													
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu
1025	1030	1035	1040												

1102-98.TXT

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
1045 1050 1055
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
1060 1065 1070
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
1075 1080 1085
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
1090 1095 1100
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
1105 1110 1115 1120
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
1125 1130 1135
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
1140 1145 1150
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
1155 1160 1165
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
1170 1175 1180
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
1185 1190 1195 1200
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
1205 1210 1215
Gly Lys

<210> 33

<211> 963

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion protein

<400> 33

Met Asn Leu Gln Pro Ile Phe Trp Ile Gly Leu Ile Ser Ser Val Cys
1 5 10 15
Cys Val Phe Ala Gln Thr Asp Glu Asn Arg Cys Leu Lys Ala Asn Ala
20 25 30
Lys Ser Cys Gly Glu Cys Ile Gln Ala Gly Pro Asn Cys Gly Trp Cys
35 40 45
Thr Asn Ser Thr Phe Leu Gln Glu Gly Met Pro Thr Ser Ala Arg Cys
50 55 60
Asp Asp Leu Glu Ala Leu Lys Lys Gly Cys Pro Pro Asp Asp Ile
65 70 75 80
Glu Asn Pro Arg Gly Ser Lys Asp Ile Lys Lys Asn Lys Asn Val Thr
85 90 95
Asn Arg Ser Lys Gly Thr Ala Glu Lys Leu Lys Pro Glu Asp Ile His
100 105 110
Gln Ile Gln Pro Gln Gln Leu Val Leu Arg Leu Arg Ser Gly Glu Pro
115 120 125
Gln Thr Phe Thr Leu Lys Phe Lys Arg Ala Glu Asp Tyr Pro Ile Asp
130 135 140
Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Glu
145 150 155 160
Asn Val Lys Ser Leu Gly Thr Asp Leu Met Asn Glu Met Arg Arg Ile
165 170 175
Thr Ser Asp Phe Arg Ile Gly Phe Gly Ser Phe Val Glu Lys Thr Val
180 185 190
Met Pro Tyr Ile Ser Thr Thr Pro Ala Lys Leu Arg Asn Pro Cys Thr
195 200 205
Ser Glu Gln Asn Cys Thr Thr Pro Phe Ser Tyr Lys Asn Val Leu Ser
210 215 220

1102-98.TXT

Leu Thr Asn Lys Gly Glu Val Phe Asn Glu Leu Val Gly Lys Gln Arg
 225 230 235 240
 Ile Ser Gly Asn Leu Asp Ser Pro Glu Gly Gly Phe Asp Ala Ile Met
 245 250 255
 Gln Val Ala Val Cys Gly Ser Leu Ile Gly Trp Arg Asn Val Thr Arg
 260 265 270
 Leu Leu Val Phe Ser Thr Asp Ala Gly Phe His Phe Ala Gly Asp Gly
 275 280 285
 Lys Leu Gly Gly Ile Val Leu Pro Asn Asp Gly Gln Cys His Leu Glu
 290 295 300
 Asn Asn Met Tyr Thr Met Ser His Tyr Tyr Asp Tyr Pro Ser Ile Ala
 305 310 315 320
 His Leu Val Gln Lys Leu Ser Glu Asn Asn Ile Gln Thr Ile Phe Ala
 325 330 335
 Val Thr Glu Glu Phe Gln Pro Val Tyr Lys Glu Leu Lys Asn Leu Ile
 340 345 350
 Pro Lys Ser Ala Val Gly Thr Leu Ser Ala Asn Ser Ser Asn Val Ile
 355 360 365
 Gln Leu Ile Ile Asp Ala Tyr Asn Ser Leu Ser Ser Glu Val Ile Leu
 370 375 380
 Glu Asn Gly Lys Leu Ser Glu Gly Val Thr Ile Ser Tyr Lys Ser Tyr
 385 390 395 400
 Cys Lys Asn Gly Val Asn Gly Thr Gly Glu Asn Gly Arg Lys Cys Ser
 405 410 415
 Asn Ile Ser Ile Gly Asp Glu Val Gln Phe Glu Ile Ser Ile Thr Ser
 420 425 430
 Asn Lys Cys Pro Lys Lys Asp Ser Asp Ser Phe Lys Ile Arg Pro Leu
 435 440 445
 Gly Phe Thr Glu Glu Val Glu Val Ile Leu Gln Tyr Ile Cys Glu Cys
 450 455 460
 Glu Cys Gln Ser Glu Gly Ile Pro Glu Ser Pro Lys Cys His Glu Gly
 465 470 475 480
 Asn Gly Thr Phe Glu Cys Gly Ala Cys Arg Cys Asn Glu Gly Arg Val
 485 490 495
 Gly Arg His Cys Glu Cys Ser Thr Asp Glu Val Asn Ser Glu Asp Met
 500 505 510
 Asp Ala Tyr Cys Arg Lys Glu Asn Ser Ser Glu Ile Cys Ser Asn Asn
 515 520 525
 Gly Glu Cys Val Cys Gly Gln Cys Val Cys Arg Lys Arg Asp Asn Thr
 530 535 540
 Asn Glu Ile Tyr Ser Gly Lys Phe Cys Glu Cys Asp Asn Phe Asn Cys
 545 550 555 560
 Asp Arg Ser Asn Gly Leu Ile Cys Gly Asn Gly Val Cys Lys Cys
 565 570 575
 Arg Val Cys Glu Cys Asn Pro Asn Tyr Thr Gly Ser Ala Cys Asp Cys
 580 585 590
 Ser Leu Asp Thr Ser Thr Cys Glu Ala Ser Asn Gly Gln Ile Cys Asn
 595 600 605
 Gly Arg Gly Ile Cys Glu Cys Gly Val Cys Lys Cys Thr Asp Pro Lys
 610 615 620
 Phe Gln Gly Gln Thr Cys Glu Met Cys Gln Thr Cys Leu Gly Val Cys
 625 630 635 640
 Ala Glu His Lys Glu Cys Val Gln Cys Arg Ala Phe Asn Lys Gly Glu
 645 650 655
 Lys Lys Asp Thr Cys Thr Gln Glu Cys Ser Tyr Phe Asn Ile Thr Lys
 660 665 670
 Val Glu Ser Arg Asp Lys Leu Pro Gln Pro Val Gln Pro Asp Pro Val
 675 680 685
 Ser His Cys Lys Glu Lys Asp Val Asp Asp Cys Trp Phe Tyr Phe Thr
 690 695 700
 Tyr Ser Val Asn Gly Asn Asn Glu Val Met Val His Val Val Glu Asn
 705 710 715 720
 Pro Glu Cys Pro Thr Gly Pro Glu Asp Pro Glu Glu Pro Lys Ser Cys

1102-98.TXT

Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
725					730								735		
740					745								750		
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
755					760								765		
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
770					775								780		
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
785					790								795		800
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
													805		815
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
													820		830
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
													835		845
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
													850		860
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
													865		880
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
													885		895
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
													900		910
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
													915		925
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
													930		940
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
													945		960
Pro	Gly	Lys													

<210> 34
 <211> 1367
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion protein

<400> 34
 Met Gly Pro Glu Arg Thr Gly Ala Ala Pro Leu Pro Leu Leu Val
 1 5 10 15
 Leu Ala Leu Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val
 20 25 30
 Gly Leu Pro Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe
 35 40 45
 Gly Tyr Ala Val Gln Gln Phe Ile Asn Pro Lys Gly Asn Trp Leu Leu
 50 55 60
 Val Gly Ser Pro Trp Ser Gly Phe Pro Glu Asn Arg Met Gly Asp Val
 65 70 75 80
 Tyr Lys Cys Pro Val Asp Leu Ser Thr Ala Thr Cys Glu Lys Leu Asn
 85 90 95
 Leu Gln Thr Ser Thr Ser Ile Pro Asn Val Thr Glu Met Lys Thr Asn
 100 105 110
 Met Ser Leu Gly Leu Ile Leu Thr Arg Asn Met Gly Thr Gly Gly Phe
 115 120 125
 Leu Thr Cys Gly Pro Leu Trp Ala Gln Gln Cys Gly Asn Gln Tyr Tyr
 130 135 140
 Thr Thr Gly Val Cys Ser Asp Ile Ser Pro Asp Phe Gln Leu Ser Ala
 145 150 155 160
 Ser Phe Ser Pro Ala Thr Gln Pro Cys Pro Ser Leu Ile Asp Val Val

1102-98.TXT

Val	Val	Cys	Asp	165	Glu	Ser	Asn	Ser	Ile	Tyr	Pro	Trp	Asp	Ala	Val	Lys
				180					185					190		
Asn	Phe	Leu	Glu	Lys	Phe	Val	Gln	Gly	Leu	Asp	Ile	Gly	Pro	Thr	Lys	
				195					200				205			
Thr	Gln	Val	Gly	Leu	Ile	Gln	Tyr	Ala	Asn	Asn	Pro	Arg	Val	Val	Phe	
				210			215				220					
Asn	Leu	Asn	Thr	Tyr	Lys	Thr	Lys	Glu	Glu	Met	Ile	Val	Ala	Thr	Ser	
				225			230			235			240			
Gln	Thr	Ser	Gln	Tyr	Gly	Gly	Asp	Leu	Thr	Asn	Thr	Phe	Gly	Ala	Ile	
				245			250			255						
Gln	Tyr	Ala	Arg	Lys	Tyr	Ala	Tyr	Ser	Ala	Ala	Ser	Gly	Gly	Arg	Arg	
				260			265				270					
Ser	Ala	Thr	Lys	Val	Met	Val	Val	Val	Thr	Asp	Gly	Glu	Ser	His	Asp	
				275			280				285					
Gly	Ser	Met	Leu	Lys	Ala	Val	Ile	Asp	Gln	Cys	Asn	His	Asp	Asn	Ile	
				290			295			300						
Leu	Arg	Phe	Gly	Ile	Ala	Val	Leu	Gly	Tyr	Leu	Asn	Arg	Asn	Ala	Leu	
				305			310			315			320			
Asp	Thr	Lys	Asn	Leu	Ile	Lys	Glu	Ile	Lys	Ala	Ile	Ala	Ser	Ile	Pro	
				325			330			335						
Thr	Glu	Arg	Tyr	Phe	Phe	Asn	Val	Ser	Asp	Glu	Ala	Ala	Leu	Leu	Glu	
				340			345			350						
Lys	Ala	Gly	Thr	Leu	Gly	Glu	Gln	Ile	Phe	Ser	Ile	Glu	Gly	Thr	Val	
				355			360			365						
Gln	Gly	Gly	Asp	Asn	Phe	Gln	Met	Glu	Met	Ser	Gln	Val	Gly	Phe	Ser	
				370			375			380						
Ala	Asp	Tyr	Ser	Ser	Gln	Asn	Asp	Ile	Leu	Met	Leu	Gly	Ala	Val	Gly	
				385			390			395			400			
Ala	Phe	Gly	Trp	Ser	Gly	Thr	Ile	Val	Gln	Lys	Thr	Ser	His	Gly	His	
				405			410			415						
Leu	Ile	Phe	Pro	Lys	Gln	Ala	Phe	Asp	Gln	Ile	Leu	Gln	Asp	Arg	Asn	
				420			425			430						
His	Ser	Ser	Tyr	Leu	Gly	Tyr	Ser	Val	Ala	Ala	Ile	Ser	Thr	Gly	Glu	
				435			440			445						
Ser	Thr	His	Phe	Val	Ala	Gly	Ala	Pro	Arg	Ala	Asn	Tyr	Thr	Gly	Gln	
				450			455			460						
Ile	Val	Leu	Tyr	Ser	Val	Asn	Glu	Asn	Gly	Asn	Ile	Thr	Val	Ile	Gln	
				465			470			475			480			
Ala	His	Arg	Gly	Asp	Gln	Ile	Gly	Ser	Tyr	Phe	Gly	Ser	Val	Leu	Cys	
				485			490			495						
Ser	Val	Asp	Val	Asp	Lys	Asp	Thr	Ile	Thr	Asp	Val	Leu	Leu	Val	Gly	
				500			505			510						
Ala	Pro	Met	Tyr	Met	Ser	Asp	Leu	Lys	Lys	Glu	Glu	Gly	Arg	Val	Tyr	
				515			520			525						
Leu	Phe	Thr	Ile	Lys	Lys	Gly	Ile	Leu	Gly	Gln	His	Gln	Phe	Leu	Glu	
				530			535			540						
Gly	Pro	Glu	Gly	Ile	Glu	Asn	Thr	Arg	Phe	Gly	Ser	Ala	Ile	Ala	Ala	
				545			550			555			560			
Leu	Ser	Asp	Ile	Asn	Met	Asp	Gly	Phe	Asn	Asp	Val	Ile	Val	Gly	Ser	
				565			570			575						
Pro	Leu	Glu	Asn	Gln	Asn	Ser	Gly	Ala	Val	Tyr	Ile	Tyr	Asn	Gly	His	
				580			585			590						
Gln	Gly	Thr	Ile	Arg	Thr	Lys	Tyr	Ser	Gln	Lys	Ile	Leu	Gly	Ser	Asp	
				595			600			605						
Gly	Ala	Phe	Arg	Ser	His	Leu	Gln	Tyr	Phe	Gly	Arg	Ser	Leu	Asp	Gly	
				610			615			620						
Tyr	Gly	Asp	Leu	Asn	Gly	Asp	Ser	Ile	Thr	Asp	Val	Ser	Ile	Gly	Ala	
				625			630			635			640			
Phe	Gly	Gln	Val	Val	Gln	Leu	Trp	Ser	Gln	Ser	Ile	Ala	Asp	Val	Ala	
				645			650			655						
Ile	Glu	Ala	Ser	Phe	Thr	Pro	Glu	Lys	Ile	Thr	Leu	Val	Asn	Lys	Asn	
				660			665			670						

1102-98.TXT

Ala Gln Ile Ile Leu Lys Leu Cys Phe Ser Ala Lys Phe Arg Pro Thr
 675 680 685
 Lys Gln Asn Asn Gln Val Ala Ile Val Tyr Asn Ile Thr Leu Asp Ala
 690 695 700
 Asp Gly Phe Ser Ser Arg Val Thr Ser Arg Gly Leu Phe Lys Glu Asn
 705 710 715 720
 Asn Glu Arg Cys Leu Gln Lys Asn Met Val Val Asn Gln Ala Gln Ser
 725 730 735
 Cys Pro Glu His Ile Ile Tyr Ile Gln Glu Pro Ser Asp Val Val Asn
 740 745 750
 Ser Leu Asp Leu Arg Val Asp Ile Ser Leu Glu Asn Pro Gly Thr Ser
 755 760 765
 Pro Ala Leu Glu Ala Tyr Ser Glu Thr Ala Lys Val Phe Ser Ile Pro
 770 775 780
 Phe His Lys Asp Cys Gly Glu Asp Gly Leu Cys Ile Ser Asp Leu Val
 785 790 795 800
 Leu Asp Val Arg Gln Ile Pro Ala Ala Gln Glu Gln Pro Phe Ile Val
 805 810 815
 Ser Asn Gln Asn Lys Arg Leu Thr Phe Ser Val Thr Leu Lys Asn Lys
 820 825 830
 Arg Glu Ser Ala Tyr Asn Thr Gly Ile Val Val Asp Phe Ser Glu Asn
 835 840 845
 Leu Phe Phe Ala Ser Phe Ser Leu Pro Val Asp Gly Thr Glu Val Thr
 850 855 860
 Cys Gln Val Ala Ala Ser Gln Lys Ser Val Ala Cys Asp Val Gly Tyr
 865 870 875 880
 Pro Ala Leu Lys Arg Glu Gln Gln Val Thr Phe Thr Ile Asn Phe Asp
 885 890 895
 Phe Asn Leu Gln Asn Leu Gln Asn Gln Ala Ser Leu Ser Phe Gln Ala
 900 905 910
 Leu Ser Glu Ser Gln Glu Glu Asn Lys Ala Asp Asn Leu Val Asn Leu
 915 920 925
 Lys Ile Pro Leu Leu Tyr Asp Ala Glu Ile His Leu Thr Arg Ser Thr
 930 935 940
 Asn Ile Asn Phe Tyr Glu Ile Ser Ser Asp Gly Asn Val Pro Ser Ile
 945 950 955 960
 Val His Ser Phe Glu Asp Val Gly Pro Lys Phe Ile Phe Ser Leu Lys
 965 970 975
 Val Thr Thr Gly Ser Val Pro Val Ser Met Ala Thr Val Ile Ile His
 980 985 990
 Ile Pro Gln Tyr Thr Lys Glu Lys Asn Pro Leu Met Tyr Leu Thr Gly
 995 1000 1005
 Val Gln Thr Asp Lys Ala Gly Asp Ile Ser Cys Asn Ala Asp Ile Asn
 1010 1015 1020
 Pro Leu Lys Ile Gly Gln Thr Ser Ser Ser Val Ser Phe Lys Ser Glu
 1025 1030 1035 1040
 Asn Phe Arg His Thr Lys Glu Leu Asn Cys Arg Thr Ala Ser Cys Ser
 1045 1050 1055
 Asn Val Thr Cys Trp Leu Lys Asp Val His Met Lys Gly Glu Tyr Phe
 1060 1065 1070
 Val Asn Val Thr Thr Arg Ile Trp Asn Gly Thr Phe Ala Ser Ser Thr
 1075 1080 1085
 Phe Gln Thr Val Gln Leu Thr Ala Ala Ala Glu Ile Asn Thr Tyr Asn
 1090 1095 1100
 Pro Glu Ile Tyr Val Ile Glu Asp Asn Thr Val Thr Ile Pro Leu Met
 1105 1110 1115 1120
 Ile Met Lys Pro Asp Glu Lys Ala Glu Val Pro Thr Asp Pro Glu Glu
 1125 1130 1135
 Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 1140 1145 1150
 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 1155 1160 1165
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

1102-98.TXT

1170 1175 1180
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
1185 1190 1195 1200
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
1205 1210 1215
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
1220 1225 1230
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
1235 1240 1245
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
1250 1255 1260
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
1265 1270 1275 1280
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
1285 1290 1295
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
1300 1305 1310
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
1315 1320 1325
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
1330 1335 1340
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
1345 1350 1355 1360
Leu Ser Leu Ser Pro Gly Lys
1365